

## CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 4/5/02Edited by: DCVerified by: DC (STIC staff)

OPE

Serial Number: 10/006,883A

F3

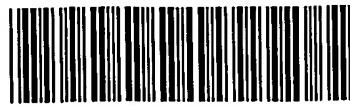
 Changed a file from non-ASCII to ASCII Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically:

ENTERED

 Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_. Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  page numbers throughout text;  other invalid text, such as \_\_\_\_\_. Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other:

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/006,883A

DATE: 04/05/2002 P.6  
TIME: 16:25:00

Input Set : A:\PTO.DC.txt  
Output Set: N:\CRF3\04052002\J006883A.raw

3 <110> APPLICANT: Kenneth W. Dobie  
5 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION  
7 <130> FILE REFERENCE: RTS-0337  
9 <140> CURRENT APPLICATION NUMBER: US/10/006,883A  
10 <141> CURRENT FILING DATE: 2001-12-05  
12 <160> NUMBER OF SEQ ID NOS: 96  
14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 20  
16 <212> TYPE: DNA  
17 <213> ORGANISM: Artificial Sequence  
19 <220> FEATURE:  
20 <223> OTHER INFORMATION: Antisense Oligonucleotide  
22 <400> SEQUENCE: 1 20  
23 tccgtcatcg ctcctcaggg  
26 <210> SEQ ID NO: 2  
27 <211> LENGTH: 20  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Artificial Sequence  
31 <220> FEATURE:  
32 <223> OTHER INFORMATION: Antisense Oligonucleotide  
34 <400> SEQUENCE: 2 20  
35 atgcattctg cccccaagga  
38 <210> SEQ ID NO: 3  
39 <211> LENGTH: 4390  
40 <212> TYPE: DNA  
41 <213> ORGANISM: Homo sapiens  
43 <220> FEATURE:  
44 <221> NAME/KEY: CDS  
45 <222> LOCATION: '(425)...(3286)  
47 <400> SEQUENCE: 3  
48 ctctagctct cagcggctgc gaagtctgta aacctggtgg ccaagtgatt gtaagtcagg 60  
50 agactttcct tcgggttctg ctttgcattt caatttcctt cggtttctgc ctgttgcattt 120  
52 aagagggttgg aattttttttt aatattttttt aacttccaaat gaaatattttt gaaatattttt 180  
54 tatggaaatc gcaggcttgg aagagacaga agcaatttcca gaaataaaattt gaaatattttt 240  
56 gattttaaaca atgttgcattt aatattttttt aacttccaaat gatgttgcattt gaaatattttt 300  
58 aaggggctgc gcagagtagc agggggccctt gagggcgcgg ccttgcattt gattttttttt 360  
60 ctgttgcattt gacacacgca gcttgcattt aatttttttt aatgttgcattt gttttttttt 420  
62 aact atg gaa gag cag cac agt gag atg gaa ata atc cca tca gag 469  
63 Met Glu Glu Gln Gly His Ser Glu Met Glu Ile Ile Pro Ser Glu 15  
64 1 5 10 15  
66 tct cac ccc cac att caa tta ctg aaa agc aat cgg gaa ctt ctg gtc 517  
67 Ser His Pro His Ile Gln Leu Leu Lys Ser Asn Arg Glu Leu Leu Val  
68 20 25 30

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71	Thr	His	Ile	Arg	Asn	Thr	Gln	Cys	Leu	Val	Asp	Asn	Leu	Leu	Lys	Asn	
72				35					40					45			
74	gac	tac	tcc	tcg	gcc	gaa	gat	gcg	gag	att	gtg	tgt	gcc	tgc	ccc	acc	613
75	Asp	Tyr	Phe	Ser	Ala	Glu	Asp	Ala	Glu	Ile	Val	Cys	Ala	Cys	Pro	Thr	
76					50				55				60				
78	cag	cct	gac	aag	gtc	cgc	aaa	att	ctg	gac	ctg	gtc	agc	aag	ggc		661
79	Gln	Pro	Asp	Lys	Val	Arg	Lys	Ile	Leu	Asp	Leu	Val	Gln	Ser	Lys	Gly	
80					65				70				75				
82	gag	gag	gtg	tcc	gag	ttc	ttc	ctc	tac	ttg	ctc	cag	caa	ctc	gca	gat	709
83	Glu	Glu	Val	Ser	Glu	Phe	Phe	Leu	Tyr	Leu	Leu	Gln	Gln	Leu	Ala	Asp	
84					80				85				90			95	
86	gcc	tac	gtg	gac	ctc	agg	cct	tgg	ctg	gag	atc	ggc	ttc	tcc	cct		757
87	Ala	Tyr	Val	Asp	Leu	Arg	Pro	Trp	Leu	Leu	Glu	Ile	Gly	Phe	Ser	Pro	
88					100				105				110				
90	tcc	ctg	ctc	act	cag	agc	aaa	gtc	gtg	gtc	aac	act	gac	cca	gtg	agc	805
91	Ser	Leu	Leu	Thr	Gln	Ser	Lys	Val	Val	Val	Asn	Thr	Asp	Pro	Val	Ser	
92					115				120				125				
94	agg	tat	acc	cag	cag	ctg	cga	cac	cat	ctg	ggc	cgt	gac	tcc	aag	ttc	
95	Arg	Tyr	Thr	Gln	Gln	Leu	Arg	His	His	Leu	Gly	Arg	Asp	Ser	Lys	Phe	
96					130				135				140				
98	gtg	ctg	tgc	tat	gcc	cag	aag	gag	gag	ctg	ctg	ctg	gag	gag	atc	tac	901
99	Val	Leu	Cys	Tyr	Ala	Gln	Lys	Glu	Glu	Leu	Leu	Leu	Glu	Glu	Ile	Tyr	
100					145				150				155				
102	atg	gac	acc	atc	atg	gag	ctg	gtt	ggc	ttc	agc	aat	gag	agc	ctg	ggc	949
103	Met	Asp	Thr	Ile	Met	Glu	Leu	Val	Gly	Phe	Ser	Asn	Glu	Ser	Leu	Gly	
104					160				165				170			175	
106	agc	ctg	aac	agc	ctg	gcc	tgc	ctc	ctg	gac	cac	acc	acc	ggc	atc	ctc	997
107	Ser	Leu	Asn	Ser	Leu	Ala	Cys	Leu	Leu	Asp	His	Thr	Thr	Gly	Ile	Leu	
108					180				185				190				
110	aat	gag	cag	ggt	gag	acc	atc	ttc	atc	ctg	ggt	gat	gct	ggg	gtg	ggc	1045
111	Asn	Glu	Gln	Gly	Glu	Thr	Ile	Phe	Ile	Leu	Gly	Asp	Ala	Gly	Val	Gly	
112					195				200				205				
114	aag	tcc	atg	ctg	cta	cag	cg	ctg	cag	agc	ctc	tgg	gcc	acg	ggc	cg	1093
115	Lys	Ser	Met	Leu	Leu	Gln	Arg	Leu	Gln	Ser	Leu	Trp	Ala	Thr	Gly	Arg	
116					210				215				220				
118	cta	gac	gca	ggg	gtc	aaa	ttc	ttc	ttc	cac	ttt	cg	tc	cg	atg	ttc	1141
119	Leu	Asp	Ala	Gly	Val	Lys	Phe	Phe	Phe	His	Phe	Arg	Cys	Arg	Met	Phe	
120					225				230				235				
122	agc	tgc	tcc	aag	gaa	agt	gac	agg	ctg	tgt	ctg	cag	gac	ctg	ctc	ttc	1189
123	Ser	Cys	Phe	Lys	Glu	Ser	Asp	Arg	Leu	Cys	Leu	Gln	Asp	Leu	Leu	Phe	
124					240				245				250			255	
126	aag	cac	tac	tgc	tac	cca	gag	cg	gac	ccc	gag	gag	gtg	ttt	gcc	ttc	1237
127	Lys	His	Tyr	Cys	Tyr	Pro	Glu	Arg	Asp	Pro	Glu	Glu	Val	Phe	Ala	Phe	
128					260				265				270				
130	ctg	ctg	cgc	ttc	ccc	cac	gtg	gcc	ctc	ttc	acc	ttc	gat	ggc	ctg	gac	1285
131	Leu	Leu	Arg	Phe	Pro	His	Val	Ala	Leu	Phe	Thr	Phe	Asp	Gly	Leu	Asp	
132					275				280				285				
134	gag	ctg	cac	tgc	gac	ttt	gac	ctg	agc	cgc	gtg	cct	gac	agc	tcc	tgc	1333

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135	Glu	Leu	His	Ser	Asp	Leu	Asp	Leu	Ser	Arg	Val	Pro	Asp	Ser	Ser	Cys
136		290				295					300					
138	ccc	tgg	gag	cct	gcc	cac	ccc	ctg	gtc	ttg	ctg	gcc	aac	ctg	ctc	agt
139	Pro	Trp	Glu	Pro	Ala	His	Pro	Leu	Val	Leu	Leu	Ala	Asn	Leu	Leu	Ser
140		305				310					315					
142	ggg	aag	ctg	ctc	aag	ggg	gct	agc	aag	ctg	ctc	aca	gcc	cgc	aca	ggc
143	Gly	Lys	Leu	Leu	Lys	Gly	Ala	Ser	Lys	Leu	Leu	Thr	Ala	Arg	Thr	Gly
144	320				325					330			335			
146	atc	gag	gtc	ccg	cgc	cag	ttc	ctg	cg	aag	aag	gtg	ctt	ctc	cgg	ggc
147	Ile	Glu	Val	Pro	Arg	Gln	Phe	Leu	Arg	Lys	Lys	Val	Leu	Leu	Arg	Gly
148		340				345					350					
150	ttc	tcc	ccc	agc	cac	ctg	cgc	tat	gcc	agg	agg	atg	ttc	ccc	gag	
151	Phe	Ser	Pro	Ser	His	Leu	Arg	Ala	Tyr	Ala	Arg	Arg	Met	Phe	Pro	Glu
152		355				360					365					
154	cgg	gcc	ctg	cag	gac	cgc	ctg	ctg	agc	cag	ctg	gag	gcc	aac	ccc	aac
155	Arg	Ala	Leu	Gln	Asp	Arg	Leu	Leu	Ser	Gln	Leu	Glu	Ala	Asn	Pro	Asn
156		370				375					380					
158	ctc	tgc	agc	ctg	tgc	tct	gtg	ccc	ctc	ttc	tgc	atc	atc	ttc	cgg	
159	Leu	Cys	Ser	Leu	Cys	Ser	Val	Pro	Leu	Phe	Cys	Trp	Ile	Ile	Phe	Arg
160		385				390					395					
162	tgc	ttc	cac	ttc	cgt	gct	gcc	ttt	gaa	ggc	tca	cca	cag	ctg	ccc	
163	Cys	Phe	Gln	His	Phe	Arg	Ala	Ala	Phe	Glu	Gly	Ser	Pro	Gln	Leu	Pro
164		400				405				410			415			
166	gac	tgc	acg	atg	acc	ctg	aca	gat	gtc	ttc	ctc	ctg	gtc	act	gag	gtc
167	Asp	Cys	Thr	Met	Thr	Leu	Thr	Asp	Val	Phe	Leu	Leu	Val	Thr	Glu	Val
168		420				425					430					
170	cat	ctg	aac	agg	atg	cag	ccc	agc	agc	ctg	gtg	cag	gg	aac	aca	cgc
171	His	Leu	Asn	Arg	Met	Gln	Pro	Ser	Ser	Leu	Val	Gln	Arg	Asn	Thr	Arg
172		435				440					445					
174	agc	cca	gtg	gag	acc	ctc	cac	gcc	gg	gac	act	ctg	tgc	tgc		
175	Ser	Pro	Val	Glu	Thr	Leu	His	Ala	Gly	Arg	Asp	Thr	Leu	Cys	Ser	Leu
176		450				455					460					
178	ggg	cag	gtg	gcc	cac	cg	gg	atg	gag	aag	agc	ctc	ttt	gtc	ttc	acc
179	Gly	Gln	Val	Ala	His	Arg	Gly	Met	Glu	Lys	Ser	Leu	Phe	Val	Phe	Thr
180		465				470					475					
182	cag	gag	gag	gtg	cag	gcc	tcc	ggg	ctg	cag	gag	aga	gac	atg	cag	ctg
183	Gln	Glu	Glu	Val	Gln	Ala	Ser	Gly	Leu	Gln	Glu	Arg	Asp	Met	Gln	Leu
184		480				485					490			495		
186	ggc	ttc	ctg	cg	gct	ttt	cg	gag	ctg	ggc	ccc	ggg	gg	gac	cag	cag
187	Gly	Phe	Leu	Arg	Ala	Leu	Pro	Glu	Leu	Gly	Pro	Gly	Gly	Asp	Gln	Gln
188		500				505					510					
190	tcc	tat	gag	ttt	ttc	cac	ctc	acc	cag	gcc	ttt	aca	gcc	ttc		
191	Ser	Tyr	Glu	Phe	Phe	His	Leu	Thr	Leu	Gln	Ala	Phe	Phe	Thr	Ala	Phe
192		515				520					525					
194	ttc	ctc	gtg	ctg	gac	gac	agg	gtg	ggc	act	cag	gag	ctg	ctc	agg	ttc
195	Phe	Leu	Val	Leu	Asp	Asp	Arg	Val	Gly	Thr	Gln	Glu	Leu	Leu	Arg	Phe
196		530				535					540					
198	ttc	cag	gag	tgg	atg	ccc	cct	gct	ggg	gca	gct	acc	acg	tcc	tgc	tat
199	Phe	Gln	Glu	Trp	Met	Pro	Pro	Ala	Gly	Ala	Ala	Thr	Thr	Ser	Cys	Tyr

RAW SEQUENCE LISTING  
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202	cct ccc ttc ctc ccg ttc cag tgc ctg cag ggc agt ggt ccg gcg cgg			2149
203	Pro Pro Phe Leu Pro Phe Gln Cys Leu Gln Gly Ser Gly Pro Ala Arg			
204	560	565	570	575
206	gaa gac ctc ttc aag aac aag gat cac ttc cag ttc acc aac ctc ttc			2197
207	Glu Asp Leu Phe Lys Asn Lys Asp His Phe Gln Phe Thr Asn Leu Phe			
208	580	585	590	
210	ctg tgc ggg ctg ttg tcc aaa gcc aaa cag aaa ctc ctg cgg cat ctg			2245
211	Leu Cys Gly Leu Leu Ser Lys Ala Lys Gln Lys Leu Leu Arg His Leu			
212	595	600	605	
214	gtg ccc gcg gca gcc ctg agg aga aag cgc aag gcc ctg tgg gca cac			2293
215	Val Pro Ala Ala Ala Leu Arg Arg Lys Arg Lys Ala Leu Trp Ala His			
216	610	615	620	
218	ctg ttt tcc agc ctg cgg ggc tac ctg aag agc ctg ccc cgc gtt cag			2341
219	Leu Phe Ser Ser Leu Arg Gly Tyr Leu Lys Ser Leu Pro Arg Val Gln			
220	625	630	635	
222	gtc gaa agc ttc aac cag gtg cag gcc atg ccc acg ttc atc tgg atg			2389
223	Val Glu Ser Phe Asn Gln Val Gln Ala Met Pro Thr Phe Ile Trp Met			
224	640	645	650	655
226	ctg cgc tgc atc tac gag aca cag agc cag aag gtg ggg cag ctg gcg			2437
227	Leu Arg Cys Ile Tyr Glu Thr Gln Ser Gln Lys Val Gly Gln Leu Ala			
228	660	665	670	
230	gcc agg ggc atc tgc gcc aac tac ctc aag ctg acc tac tgc aac gcc			2485
231	Ala Arg Gly Ile Cys Ala Asn Tyr Leu Lys Leu Thr Tyr Cys Asn Ala			
232	675	680	685	
234	tgc tcg gcc gac tgc agc gcc ctc tcc ttc gtc ctg cat cac ttc ccc			2533
235	Cys Ser Ala Asp Cys Ser Ala Leu Ser Phe Val Leu His His Phe Pro			
236	690	695	700	
238	aag cgg ctg gcc cta gac cta gac aac aac aat ctc aac gac tac ggc			2581
239	Lys Arg Leu Ala Leu Asp Leu Asp Asn Asn Leu Asn Asp Tyr Gly			
240	705	710	715	
242	gtg cgg gag ctg cag ccc tgc ttc agc cgc ctc act gtt ctc aga ctc			2629
243	Val Arg Glu Leu Gln Pro Cys Phe Ser Arg Leu Thr Val Leu Arg Leu			
244	720	725	730	735
246	agc gta aac cag atc act gac ggt ggg gta aag gtg cta agc gaa gag			2677
247	Ser Val Asn Gln Ile Thr Asp Gly Gly Val Lys Val Leu Ser Glu Glu			
248	740	745	750	
250	ctg acc aaa tac aaa att gtg acc tat ttg ggt tta tac aac aac cag			2725
251	Leu Thr Lys Tyr Lys Ile Val Thr Tyr Leu Gly Leu Tyr Asn Asn Gln			
252	755	760	765	
254	atc acc gat gtc gga gcc agg tac gtc acc aaa atc ctg gat gaa tgc			2773
255	Ile Thr Asp Val Gly Ala Arg Tyr Val Thr Lys Ile Leu Asp Glu Cys			
256	770	775	780	
258	aaa ggc ctc acg cat ctt aaa ctg gga aaa aac aaa ata aca agt gaa			2821
259	Lys Gly Leu Thr His Leu Lys Leu Gly Lys Asn Lys Ile Thr Ser Glu			
260	785	790	795	
262	gga ggg aag tat ctc gcc ctg gct gtg aag aac agc aaa tca atc tct			2869
263	Gly Gly Lys Tyr Leu Ala Leu Ala Val Lys Asn Ser Lys Ser Ile Ser			
264	800	805	810	815

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266 gag gtt ggg atg tgg ggc aat caa gtt ggg gat gaa gga gca aaa gcc	2917
267 Glu Val Gly Met Trp Gly Asn Gln Val Gly Asp Glu Gly Ala Lys Ala	
268 820 825 830	
270 ttc gca gag gct ctg cgg aac cac ccc agc ttg acc acc ctg agt ctt	2965
271 Phe Ala Glu Ala Leu Arg Asn His Pro Ser Leu Thr Thr Leu Ser Leu	
272 835 840 845	
274 gcg tcc aac ggc atc tcc aca gaa gga gga aag agc ctt gcg agg gcc	3013
275 Ala Ser Asn Gly Ile Ser Thr Glu Gly Gly Lys Ser Leu Ala Arg Ala	
276 850 855 860	
278 ctg cag cag aac acg tct cta gaa ata ctg tgg ctg acc caa aat gaa	3061
279 Leu Gln Gln Asn Thr Ser Leu Glu Ile Leu Trp Leu Thr Gln Asn Glu	
280 865 870 875	
282 ctc aac gat gaa gtg gca gag agt ttg gca gaa atg ttg aaa gtc aac	3109
283 Leu Asn Asp Glu Val Ala Glu Ser Leu Ala Glu Met Leu Lys Val Asn	
284 880 885 890 895	
286 cag acg tta aag cat tta tgg ctt atc cag aat cag atc aca gct aag	3157
287 Gln Thr Leu Lys His Leu Trp Leu Ile Gln Asn Gln Ile Thr Ala Lys	
288 900 905 910	
290 ggg act gcc cag ctg gca gat gcg tta cag agc aac act ggc ata aca	3205
291 Gly Thr Ala Gln Leu Ala Asp Ala Leu Gln Ser Asn Thr Gly Ile Thr	
292 915 920 925	
294 gag att tgc cta aat gga aac ctg ata aaa cca gag gag gcc aaa gtc	3253
295 Glu Ile Cys Leu Asn Gly Asn Leu Ile Lys Pro Glu Glu Ala Lys Val	
296 930 935 940	
298 tat gaa gat gag aag cgg att atc tgt ttc tga gaggatgctt tcctgttcat	3306
299 Tyr Glu Asp Glu Lys Arg Ile Ile Cys Phe	
300 945 950	
302 ggggttttg ccctggagcc tcagcagcaa atgccactct gggcagtctt ttgtgtcagt	3366
304 gtcttaagg ggcctgcgca ggcgggacta tcagggatcc actgcctcca ttagtgcagc	3426
306 cagttcctg tgcagaaggt ctggtcggca aactccctaa gtacccgcta caattctgca	3486
308 gaaaaagaat gtgtcttgcg agctgttgcgtt gttacagtaa atacactgtg aagagacttt	3546
310 attgcctatt ataattattt ttatctgaag cttagaggaat aaagctgtga gcaaacagag	3606
312 gaggccagcc tcacccatt ccaacacccg ccatagggac caacgggagc gagttggca	3666
314 ccgctttt cattgaagag ttgaggatgt ggcacaaagt tggtgccaaat cttcttgaat	3726
316 aaaacgtgtt tgatggatta gtattatacc tgaatattt tcttccttct cagcactttc	3786
318 ccatgtattt atactggtcc cacttcacag ctggagacac cggagttatgt gcagtgtgg	3846
320 atttgactcc tccaagggtt tggaaatgt taatgtcaag gaaaggatgc accacgggct	3906
322 ttaattttta atcctggagt ctcactgtct gctggcaaag atagagaatg ccctcagctc	3966
324 ttagctggc taagaatgac gatgccttca aaatgtctgt tccactcagg gcttcttcctc	4026
326 tgctaggcta ccctccctca gaaggctgtag taccatgggc tacagtgtct ggccttggga	4086
328 agaagtgatt ctgtccctcc aaagaaatag ggcatggctt gcccctgtgg ccctggcatc	4146
330 caaatggctg ctttgcctc ctttaccccg tgaagagggg aagtctcttc ctgcctccca	4206
332 agcagctgaa gggactaa acggcgccca agactcagg gatcggctgg gaactggcc	4266
334 agcagagcat gttggacacc ccccaccatg gtggctgtt ggtggctgtt ccatgagggt	4326
336 ggggtgata ctactagatc acttgtctc ttgcccgtctt atttgttaat aaaatactga	4386
338 aaac	4390
341 <210> SEQ ID NO: 4	
342 <211> LENGTH: 19	
343 <212> TYPE: DNA	

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 38  
Seq#:12; Xaa Pos. 11  
Seq#:14; N Pos. 8  
Seq#:15; N Pos. 425,426,427,428,429,430,431,432,433,434,435,436,437,438,439  
Seq#:15; N Pos. 440,441,442,443,444,445,446,447,448,449,450,451,452,453,454  
Seq#:15; N Pos. 455,456,457,458,459,460,461,462,463,464,465,466,467,468,469  
Seq#:15; N Pos. 470,471,472,473,474,475,476,477,478,479,480,481,482,483,484  
Seq#:15; N Pos. 485,486,487,488,489,490,491,492,493,494,495,496,497,498,499  
Seq#:15; N Pos. 500,501,502,503,504,505,506,507,508,509,510,511,512,513,514  
Seq#:15; N Pos. 515,516,517,518,519,520,521,522,523,524  
Seq#:95; N Pos. 72  
Seq#:96; N Pos. 1394

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,883A

DATE: 04/05/2002

TIME: 16:25:01

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\04052002\J006883A.raw

L:419 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:1157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:1162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:1337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48  
L:1358 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1359 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:  
L:1372 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:1377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
L:1395 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:1400 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:1410 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:1415 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:1425 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:1435 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:1452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:420  
L:1453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:480  
L:3019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:60  
L:3126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:96 after pos.:1380